Evolutionary History of Pearl Millet (Pennisetum glaucum [L.] R. Br.) and Selection on Flowering Genes since Its Domestication

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Auteur	Clotault, Jérémy [1], Thuillet, Anne-Céline [2], Buiron, Marylène [3], De Mita, Stéphane [4], Couderc, Marie [5], Haussmann, Bettina IG [6], Mariac, Cédric [7], Vigouroux, Yves [8]
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Résumé en anglais	The plant domestication process is associated with considerable modifications of plant phenotype. The identification of the genetic basis of this adaptation is of great interest for evolutionary biology. One of the methods used to identify such genes is the detection of signatures of selection. However, domestication is generally associated with major demographic effects. It is therefore crucial to disentangle the effects of demography and selection on diversity. In this study, we investigated selection in a flowering time pathway during domestication of pearl millet. We first used a random set of 20 genes to model pearl millet domestication using approximate Bayesian computation. This analysis showed that a model with exponential growth and wild–cultivated gene flow was well supported by our data set. Under this model, the domestication date of pearl millet is estimated at around 4,800 years ago. We assessed selection in 15 pearl millet DNA sequences homologous to flowering time genes and showed that these genes underwent selection more frequently than expected. We highlighted significant signatures of selection in six pearl millet flowering time genes associated with domestication or improvement of pearl millet. Moreover, higher deviations from neutrality were found for circadian clock–associated genes. Our study provides new insights into the domestication process of pearl millet and shows that a category of genes of the flowering pathway were preferentially selected during pearl millet domestication.

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